

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,258

Source: PCF

Date Processed by STIC: 1/24/06

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PCT

RAW SEQUENCE LISTING

DATE: 01/24/2006

PATENT APPLICATION: US/10/524,258

TIME: 10:13:32

Input Set : A:\2005-09-21 1599-0276PUS1.ST25.txt

Output Set: N:\CRF4\01052006\J524258.raw

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3 <110> APPLICANT: KOH, Sang-Seok et al.
5 <120> TITLE OF INVENTION: GENE FAMILIES ASSOCIATED WITH STOMACH CANCER
7 <130> FILE REFERENCE: 1599-0276PUS1
9 <140> CURRENT APPLICATION NUMBER: US 10/524,258
10 <141> CURRENT FILING DATE: 2005-02-11
12 <150> PRIOR APPLICATION NUMBER: PCT/KR03/01653
13 <151> PRIOR FILING DATE: 2003-08-14
15 <160> NUMBER OF SEQ ID NOS: 10
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 578
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (155)..(418)
25 <223> OTHER INFORMATION: Gene LBFL302, Clone BC4
27 <400> SEQUENCE: 1
28 cggacgcgtg gggttcgaacg ttcggactga gggtttttctg cctgaagaag cgtcatacgg      60
30 accggattgt tttcgcgtggc ccagtgtccc cggagcttgt gtgcgataca gagagcacct      120
32 cggaagctga ggcagctggt acttgacaga gagg          atg gcg ctg tcg acc      169
33                                     Met Ala Leu Ser Thr
34                                     1          5
36 ata gtc tcc cag agg aag cag ata aag cgg aag gct ccc cgt ggc ttt      217
37 Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe
38             10             15             20
40 cta aag cga gtc ttc aag cga aag aag cct caa ctt cgt ctg gag aaa      265
41 Leu Lys Arg Val Phe Lys Arg Lys Lys Pro Gln Leu Arg Leu Glu Lys
42             25             30             35
44 agt ggt gac tta ttg gtc cat ctg aac tgt tta ctg ttt gtt cat cga      313
45 Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu Leu Phe Val His Arg
46             40             45             50
48 tta gca gaa gag tcc agg aca aac gct tgt gcg agt aaa tgt aga gtc      361
49 Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala Ser Lys Cys Arg Val
50             55             60             65
52 att aac aag gag cat gta ctg gcc gca gca aag gta att cta aag aag      409
53 Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys Val Ile Leu Lys Lys
54             70             75             80             85
56 agc aga ggt          ta gaagtcaaag aacatattct tgaaagttat gatgcattct      460
57 Ser Arg Gly
59 tttgggtggt aacagatcat aaagacattt ttacacatc agttaatatg ggattattaa      520
61 atattggcta taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      578
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 88

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66 <212> TYPE: PRT
67 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
70 Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys
71   1           5           10           15
73 Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys Arg Lys Lys Pro Gln
74           20           25           30
76 Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu
77           35           40           45
79 Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala
80           50           55           60
82 Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys
83   65           70           75           80
85 Val Ile Leu Lys Lys Ser Arg Gly
86           85
89 <210> SEQ ID NO: 3
90 <211> LENGTH: 531
91 <212> TYPE: DNA
92 <213> ORGANISM: Homo sapiens
94 <220> FEATURE:
95 <221> NAME/KEY: CDS
96 <222> LOCATION: (139)..(402)
97 <223> OTHER INFORMATION: Gene LBFL302, Clone BC7
100 <400> SEQUENCE: 3
101 cccacgcgctc cggaggtttt tctgcctgaa gaagcgtcat acggaccgga ttgttttcgc      60
103 tggcccagtg tccccggagc ttgtgtgcga tacagagagc acctcggaag ctgaggcagc      120
105 tgggtacttga cagagagg  atg gcg ctg tgc acc ata gtc tcc cag agg aag      171
106           Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys
107           1           5           10
109 cag ata aag cgg aag gct ccc cgt ggc ttt cta aag cga gtc ttc aag      219
110 Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys
111           15           20           25
113 cta aag aag cct caa ctt cgt ctg gag aaa agt ggt gac tta ttg gtc      267
114 Leu Lys Lys Pro Gln Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val
115           30           35           40
117 cat ctg aac tgt tta ctg ttt gtt cat cga tta gca gaa gag tcc agg      315
118 His Leu Asn Cys Leu Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg
119           45           50           55
121 aca aac gct tgt gcg agt aaa tgt aga gtc att aac aag gag cat gta      363
122 Thr Asn Ala Cys Ala Ser Lys Cys Arg Val Ile Asn Lys Glu His Val
123   60           65           70           75
125 ctg gcc gca gca aag gta att cta aag aag agc aga ggt  tagaagtc      410
126 Leu Ala Ala Ala Lys Val Ile Leu Lys Lys Ser Arg Gly
127           80           85
129 aaagaacata ttcttgaaag ttatgatgca ttcttttggg tggtaacaga tcataaagac      470
131 attttttaca catcagttaa tatgggatta ttaaattatt gatataaaaa aaaaaaaaaa      530
133 a                                                                                   531
136 <210> SEQ ID NO: 4
137 <211> LENGTH: 88

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138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapiens
141 <400> SEQUENCE: 4
142 Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys
143   1           5           10           15
145 Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys Leu Lys Lys Pro Gln
146           20           25           30
148 Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu
149           35           40           45
151 Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala
152           50           55           60
154 Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys
155           65           70           75           80
157 Val Ile Leu Lys Lys Ser Arg Gly
158           85
161 <210> SEQ ID NO: 5
162 <211> LENGTH: 2067
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (32)..(1384)
169 <223> OTHER INFORMATION: Clone GE6
172 <400> SEQUENCE: 5
173 cccgggctgc caggcgccca gctgtgccca g          atg gat ggg aca gag          46
174                                     Met Asp Gly Thr Glu
175                                     1          5
177 acc cgg cag cgg agg ctg gac agc tgt ggc aag cca ggg gag ctg ggg          94
178 Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys Pro Gly Glu Leu Gly
179           10           15           20
181 ctt cct cac ccc ctc agc aca gga gga ctc cct gta gcc tca gaa gat          142
182 Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro Val Ala Ser Glu Asp
183           25           30           35
185 gga gct ctc agg gcc cct gag agc caa agc gtg acc ccc aag cca ctg          190
186 Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val Thr Pro Lys Pro Leu
187           40           45           50
189 gag act gag cct agc agg gag acc gcc tgg tcc ata ggc ctt cag gtg          238
190 Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser Ile Gly Leu Gln Val
191           55           60           65
193 acc gtg ccc ttc atg ttt gca ggc ctg gga ctg tcc tgg gcc ggc atg          286
194 Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu Ser Trp Ala Gly Met
195           70           75           80           85
197 ctt ctg gac tat ttc cag gcc aac act gga caa att gat gac ccc cag          334
198 Leu Leu Asp Tyr Phe Gln Ala Asn Thr Gly Gln Ile Asp Asp Pro Gln
199           90           95           100
201 gag cag cac aga gtc atc agc agc aac ctg gcc ctc atc cag gtg cag          382
202 Glu Gln His Arg Val Ile Ser Ser Asn Leu Ala Leu Ile Gln Val Gln
203           105           110           115
205 gcc act gtc gtg ggg ctc ttg gct gct gtg gct gcg ctg ctg ttg ggc          430

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206	Ala	Thr	Val	Val	Gly	Leu	Leu	Ala	Ala	Val	Ala	Ala	Leu	Leu	Leu	Gly	
207			120					125					130				
209	gtg	gtg	tct	cga	gag	gaa	gtg	gat	gtc	gcc	aag	gtg	gag	ttg	ctg	tgt	478
210	Val	Val	Ser	Arg	Glu	Glu	Val	Asp	Val	Ala	Lys	Val	Glu	Leu	Leu	Cys	
211			135					140					145				
213	gcc	agc	agt	gtc	ctc	act	gcc	ttc	ctt	gca	gcc	ttt	gcc	ctg	ggg	gtg	526
214	Ala	Ser	Ser	Val	Leu	Thr	Ala	Phe	Leu	Ala	Ala	Phe	Ala	Leu	Gly	Val	
215	150						155					160				165	
217	ctg	atg	gtc	tgt	ata	gtg	att	ggg	gct	cga	aag	ctc	ggg	gtc	aac	cca	574
218	Leu	Met	Val	Cys	Ile	Val	Ile	Gly	Ala	Arg	Lys	Leu	Gly	Val	Asn	Pro	
219					170					175					180		
221	gac	aac	att	gcc	acg	ccc	att	gca	gcc	agc	ctg	gga	gac	ctc	atc	aca	622
222	Asp	Asn	Ile	Ala	Thr	Pro	Ile	Ala	Ala	Ser	Leu	Gly	Asp	Leu	Ile	Thr	
223				185						190					195		
225	ctg	tcc	att	ctg	gct	ttg	gtt	agc	agc	ttc	ttc	tac	aga	cac	aaa	gat	670
226	Leu	Ser	Ile	Leu	Ala	Leu	Val	Ser	Ser	Phe	Phe	Tyr	Arg	His	Lys	Asp	
227			200					205					210				
229	agt	cgg	tat	ctg	acg	ccg	ctg	gtc	tgc	ctc	agc	ttt	gcg	gct	ctg	acc	718
230	Ser	Arg	Tyr	Leu	Thr	Pro	Leu	Val	Cys	Leu	Ser	Phe	Ala	Ala	Leu	Thr	
231			215				220					225					
233	cca	gtg	tgg	gtc	ctc	att	gcc	aag	cag	agc	cca	ccc	atc	gtg	aag	atc	766
234	Pro	Val	Trp	Val	Leu	Ile	Ala	Lys	Gln	Ser	Pro	Pro	Ile	Val	Lys	Ile	
235	230				235					240					245		
237	ctg	aag	ttt	ggc	tgg	ttc	cca	atc	atc	ctg	gcc	atg	gtc	atc	agc	agt	814
238	Leu	Lys	Phe	Gly	Trp	Phe	Pro	Ile	Ile	Leu	Ala	Met	Val	Ile	Ser	Ser	
239					250					255					260		
241	ttc	gga	gga	ctc	atc	ttg	agc	aaa	acc	ggt	tct	aaa	cag	cag	tac	aaa	862
242	Phe	Gly	Gly	Leu	Ile	Leu	Ser	Lys	Thr	Val	Ser	Lys	Gln	Gln	Tyr	Lys	
243				265						270					275		
245	ggc	atg	gcg	ata	ttt	acc	ccc	gtc	ata	tgt	ggg	ggt	ggg	ggc	aat	ctg	910
246	Gly	Met	Ala	Ile	Phe	Thr	Pro	Val	Ile	Cys	Gly	Val	Gly	Gly	Asn	Leu	
247			280					285					290				
249	gtg	gcc	att	cag	acc	agc	cga	atc	tca	acc	tac	ctg	cac	atg	tgg	agt	958
250	Val	Ala	Ile	Gln	Thr	Ser	Arg	Ile	Ser	Thr	Tyr	Leu	His	Met	Trp	Ser	
251			295				300					305					
253	gca	cct	ggc	gtc	ctg	ccc	ctc	cag	atg	aag	aaa	ttc	tgg	ccc	aac	ccg	1006
254	Ala	Pro	Gly	Val	Leu	Pro	Leu	Gln	Met	Lys	Lys	Phe	Trp	Pro	Asn	Pro	
255	310				315					320					325		
257	tgt	tct	act	ttc	tgc	acg	tca	gaa	atc	aat	tcc	atg	tca	gct	cga	gtc	1054
258	Cys	Ser	Thr	Phe	Cys	Thr	Ser	Glu	Ile	Asn	Ser	Met	Ser	Ala	Arg	Val	
259				330						335					340		
261	ctg	ctc	ttg	ctg	gtg	gtc	cca	ggc	cat	ctg	att	ttc	ttc	tac	atc	atc	1102
262	Leu	Leu	Leu	Leu	Val	Val	Pro	Gly	His	Leu	Ile	Phe	Phe	Tyr	Ile	Ile	
263				345					350					355			
265	tac	ctg	gtg	gag	ggg	cag	tca	gtc	ata	aac	agc	cag	acc	ttt	gtg	gtg	1150
266	Tyr	Leu	Val	Glu	Gly	Gln	Ser	Val	Ile	Asn	Ser	Gln	Thr	Phe	Val	Val	
267			360					365					370				
269	ctc	tac	ctg	ctg	gca	ggc	ctg	atc	cag	gtg	aca	atc	ctg	tac	ctg		1198
270	Leu	Tyr	Leu	Leu	Ala	Gly	Leu	Ile	Gln	Val	Thr	Ile	Leu	Leu	Tyr	Leu	

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271      375      380      385
273 gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc ctg gat cct gac      1246
274 Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala Leu Asp Pro Asp
275 390      395      400      405
277 aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac ctg ctc ggt act      1294
278 Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp Leu Leu Gly Thr
279      410      415      420
281 ggc ctc ctg gca ctc tgc ttt ttc act gac tgg cta ctg aag agc aag      1342
282 Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp Leu Leu Lys Ser Lys
283      425      430      435
285 gca gag ctg ggt ggc atc tca gaa ctg gca tct gga cct ccc      taactg      1390
286 Ala Glu Leu Gly Gly Ile Ser Glu Leu Ala Ser Gly Pro Pro
287      440      445      450
289 ggccccgctg gtcccatctg ctccattagaa tttcctctca catcagtggg atacagaatt      1450
291 cagtttctcc cttgccaggt ccttgggatg gttgaccctt gcctctgcag tagccttttg      1510
293 tgagtctgct aaggtagctc tcacacacct cggctctggg gttgatacct gagcctgcaa      1570
295 tagagccctg aaatcaagag catggcttga gtgtgtgaat atgatgtgtg cacatgctta      1630
297 atgagcgtgc aagtgtgcac acgtttgtgg agaggagggt gttctggcct gagaaggtaa      1690
299 agaagaggca tgtccagtat gctttgcagg gtgtgtttgc tcttttccat gcccatgcaa      1750
301 cccagattgg ggtggagcag gaaggagctc ttttctgttc ccaagcctca gaactcttga      1810
303 gctgtggcct acttgctgtc ttcaccaggt tcaagctccg tgggccacac tgctgctgtg      1870
305 ccaagaaggt gtacagcctc cccaggatgg ggcctcatac aacccttcat ctgcactcaa      1930
307 catttaatcg tgccttgct gtctttttat tttccttttt gtttggttagc aaaaacctct      1990
309 atttagattt caataatcag agaagtgtaa aataaaacag attatattgt aaaaaaaaaa      2050
311 aaaaaaaaaa aaaaaaaaaa      2067
314 <210> SEQ ID NO: 6
315 <211> LENGTH: 451
316 <212> TYPE: PRT
317 <213> ORGANISM: Homo sapiens
319 <400> SEQUENCE: 6
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321 1 5 10 15
323 Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
324 20 25 30
326 Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
327 35 40 45
329 Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
330 50 55 60
332 Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
333 65 70 75 80
335 Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln Ala Asn Thr Gly Gln
336 85 90 95
338 Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser Ser Asn Leu Ala
339 100 105 110
341 Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu Ala Val Ala
342 115 120 125
344 Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val Asp Val Ala Lys
345 130 135 140
347 Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala Phe Leu Ala Ala

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